

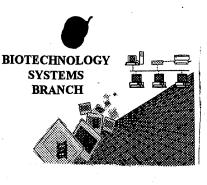
#19

2002

600/2900



RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/517,466C	MAY 01
Source:	1600	
Date Processed by STIC:	4/18/2002	TECH CENTER 1

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- Hand Carry directly to:
 U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
 - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/5/7,466C
ATTN: NEW RULES CASES	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. RECEIVEI
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. MAY 0 1 2002
S Variable Length	Sequence(s) Scontain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8 Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001



1634

RAW SEQUENCE LISTING DATE: 04/24/2002 PATENT APPLICATION: US/09/517,466C TIME: 07:44:39

Input Set : A:\09424680003seqlist ascii Output Set: N:\CRF3\04242002\I517466C.raw

Does Not Comply Needec

		1 /ozz 5 /0 22 42 002 /1317 400C. 1aw	Does Not Comply
5	<110>	APPLICANT: Hartley, James L.	Corrected Diskette Needec
7		Brasch, Michael A.	pp4-6
9		Temple, Gary F.	na 4-6
11		Cheo, David	
15	<120>	TITLE OF INVENTION: Compositions and Methods for Use i	n Recombinational
16		Cloning of Nucleic Acids	.n Recombinational
20	<130>	FILE REFERENCE: 0942.4680003	
24	<140>	CURRENT APPLICATION NUMBER: 09/517,466C	RECEIVED
26	<141>	CURRENT FILING DATE: 2000-03-02	RECEIVED
30	<150>	PRIOR APPLICATION NUMBER: US 60/122,389	
32	<151>	PRIOR FILING DATE: 1999-03-02	MAY 0 1 2002
36	<150>	PRIOR APPLICATION NUMBER: US 60/126,049	
38	<151>	PRIOR FILING DATE: 1999-03-23	TECH CENTER 1600/2900
42	<150>	PRIOR APPLICATION NUMBER: US 60/136,744	TECH CENTER 100012
44	<151>	PRIOR FILING DATE: 1999-05-28	
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		LENGTH: 25	
		TYPE: DNA	
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		FEATURE:	
68	<223>	OTHER INFORMATION: attB1 site	
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/1	acaagt	ttgt acaaaaagc aggct	25
		SEQ ID NO: 2	
		LENGTH: 25	
		TYPE: DNA	
00	<213>	ORGANISM: Artificial Sequence FEATURE:	
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		Cttt cttgtacaaa gtggt	
		SEQ ID NO: 3	25
		LENGTH: 233	
		TYPE: DNA	
		ORGANISM: Artificial Sequence	
		FEATURE:	
		OTHER INFORMATION: attP1 site	
106	<400>	SEQUENCE: 3	
		gtcac taataccatc taagtagttg attcatagtg actggatatg ttgte	m++++> 60
109	cagta	ttatg tagtctgttt tttatgcaaa atctaattta atatattgat attt	gtttta 60
111	tttta	cgttt ctcgttcagc ttttttgtac aaagttggca ttataaaaaa gcat	atatca 120
		Jerran adda godi	tgctca 180





RAW SEQUENCE LISTING DATE: 04/24/2002 PATENT APPLICATION: US/09/517,466C TIME: 07:44:39

Input Set : A:\09424680003seqlist ascii
Output Set: N:\CRF3\04242002\I517466C.raw

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126	<220> FEATURE:	
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	tgctttctta taatgccaac tttgtacaag aaagctgaac gagaaacgta aaatgatata	120
135	aatatcaata tattaaatta gattttgcat aaaaaacaga ctacataata ctgtaaaaca	180
137	caacatatcc agtcactatg aatcaactac ttagatggta ttagtgacct gta	233
140	<210> SEQ ID NO: 5	
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146	<213> ORGANISM: Artificial Sequence	
	<220> FEATURE:	
	<223> OTHER INFORMATION: attL1	
	<400> SEQUENCE: 5	
	acaagtttgt acaaaaaagc tgaacgagaa acgtaaaatg atataaatat caatatatta	60
	aattagattt tgcataaaaa acagactaca taatactgta aaacacaaca tatccagtca	120
	ctatg	125
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	<212> TYPE: DNA	
	<213> ORGANISM: Artificial Sequence <a><a><220> FEATURE:	
	<223> OTHER INFORMATION: attL2	
	<pre><223> OTHER INFORMATION: &CCU2 <400> SEQUENCE: 6</pre>	
	gcaggtcgac catagtgact ggatatgttg tgttttacag tattatgtag tctgtttttt	60
	atgcaaaatc taatttaata tattgatatt tatatcattt tacgtttctc gttcagcttt	120
	cttgtacaaa gtggt	135
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	<220> FEATURE:	
196	<223> OTHER INFORMATION: attr1	
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	<210> SEQ ID NO: 8	
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	<212> TYPE: DNA	
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	<400> SEQUENCE: 8	C O
219	caaataatga ttttattttg actgatagtg acctgttcgt tgcaacaaat tgataagcaa	60



RAW SEQUENCE LISTING DATE: 04/24/2002 PATENT APPLICATION: US/09/517,466C TIME: 07:44:39

Input Set : A:\09424680003seqlist ascii
Output Set: N:\CRF3\04242002\I517466C.raw

221		-
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	<211> LENGIH: 15 <212> TYPE: DNA	
	<213> ORGANISM: Artificial Sequence <220> FEATURE:	
	<pre><223> OTHER INFORMATION: 15 bp core region of attB, attP, attL at </pre>	nd attR
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	<210> SEQ ID NO: 10	
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	<212> TYPE: DNA	
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	<220> FEATURE:	
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	<400> SEQUENCE: 11	
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	<213> ORGANISM: Artificial Sequence	
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	<220> FEATURE:	
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/517,466C

DATE: 04/24/2002 TIME: 07:44:39

Input Set : A:\09424680003seqlist ascii Output Set: N:\CRF3\04242002\I517466C.raw

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      336 <212> TYPE: DNA
      338 <213> ORGANISM: Artificial Sequence
      342 <220> FEATURE:
      344 <223> OTHER INFORMATION: attB2(-1) Oligonucleotide Primer
      346 <220> FEATURE:
                                        n can only represent a single huchotide
      348 <221> NAME/KEY: misc_feature
      350 <222> LOCATION: (25)..(25)
      352 <223> OTHER INFORMATION: (n at the 3' end of the primer represents a target-specific
               sequence of any length
      357 <400> SEQUENCE: 15
                                                   ( see item 5 on Eva Summan
 W--> 358 cccagctttc ttgtacaaag tggtm
      361 <210> SEQ ID NO: 16
      363 <211> LENGTH: 24
      365 <212> TYPE: DNA
      367 <213> ORGANISM: Artificial Sequence
      371 <220> FEATURE:
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     375 <220> FEATURE:
     377 <221> NAME/KEY: misc_feature
     379 <222> LOCATION: (24)..(24)
     381 <223> OTHER INFORMATION: n at the 3' end of the primer represents a target-specific
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                                       same eno
     386 <400> SEQUENCE: 16
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                                                                               24
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     392 <211> LENGTH: 23
     394 <212> TYPE: DNA
     396 <213> ORGANISM: Artificial Sequence
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     404 <220> FEATURE:
     406 <221> NAME/KEY: misc_feature
     408 <222> LOCATION: (23)..(23)
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     415 <400> SEQUENCE: 17
                                         same
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     419 <210> SEQ ID NO: 18
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     421 <211> LENGTH: 22
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    425 <213> ORGANISM: Artificial Sequence
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    433 <220> FEATURE:
    435 <221> NAME/KEY: misc_feature
    437 <222> LOCATION: (22)..(22)
    439 <223> OTHER INFORMATION: n at the 3' end of the primer represents a target-specific
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/517,466C

DATE: 04/24/2002 TIME: 07:44:39

Input Set : A:\09424680003seqlist ascii
Output Set: N:\CRF3\04242002\I517466C.raw

440 sequence of any length 444 <400> SEQUENCE: 18 W--> 445 agetttettg tacaaagtgg fn 22 448 <210> SEQ ID NO: 19 450 <211> LENGTH: 26 452 <212> TYPE: DNA 454 <213> ORGANISM: Artificial Sequence 458 <220> FEATURE: 460 <223> OTHER INFORMATION: attB1- and attB2-derived Oligonucleotide Primer 462 <220> FEATURE: 464 <221> NAME/KEY: misc_feature 466 <222> LOCATION: (26)..(26) 468 <223> OTHER INFORMATION: n at the 3' end of the primer represents a target-specific sequence of any length 473 <400> SEQUENCE: 19 W--> 474 acaagtttgt acaaaaaagc aggctn 26 477 <210> SEQ ID NO: 20 479 <211> LENGTH: 26 481 <212> TYPE: DNA 483 <213> ORGANISM: Artificial Sequence 487 <220> FEATURE: 489 <223> OTHER INFORMATION: attB1- and attB2-derived Oligonucleotide Primer 491 <220> FEATURE: 493 <221> NAME/KEY: misc_feature 495 <222> LOCATION: (26)..(26) 497 <223> OTHER INFORMATION: n at the 3' end of the primer represents a target-specific 498 sequence of any length 502 <400> SEQUENCE: 20 W--> 503 accaetttgt acaagaaage tgggtn 26 506 <210> SEQ ID NO: 21 508 <211> LENGTH: 19 510 <212> TYPE: DNA 512 <213> ORGANISM: Artificial Sequence 516 <220> FEATURE: 518 <223> OTHER INFORMATION: attB1- and attB2-derived Oligonucleotide Primer 520 <220> FEATURE: 522 <221> NAME/KEY: misc_feature 524 <222> LOCATION: (19)..(19) 526 <223> OTHER INFORMATION: n at the 3' end of the primer represents a target-specific 527 sequence of any length 531 <400> SEQUENCE: 21 W--> 532 tgtacaaaaa agcaggctn sane 19 535 <210> SEQ ID NO: 22 537 <211> LENGTH: 19 539 <212> TYPE: DNA 541 <213> ORGANISM: Artificial Sequence 545 <220> FEATURE: 547 <223> OTHER INFORMATION: attB1- and attB2-derived Oligonucleotide Primer 549 <220> FEATURE:

The types of errors shown exist throughout the Securence Listing. Please check subsequent sequences for similar errors.

The types of errors shown exist throughout the Control Listing, Please check subsequent seque for similar errors.



RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/09/517,466C

DATE: 04/24/2002 TIME: 07:44:40

Input Set : A:\09424680003seqlist ascii
Output Set: N:\CRF3\04242002\I517466C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the $\langle 220 \rangle$ to $\langle 223 \rangle$ fields of each sequence which presents at least one n or Xaa.

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Seq#:15; N Pos. 25
 Seq#:16; N Pos. 24
Seq#:17; N Pos. 23
 Seq#:18; N Pos. 22
Seq#:19; N Pos. 26
Seq#:20; N Pos. 26
Seq#:21; N Pos. 19
Seq#:22; N Pos. 19
Seq#:23; N Pos. 16
Seq#:24; N Pos. 16
Seq#:25; N Pos. 13
Seq#:26; N Pos. 13
Seq#:27; N Pos. 12
Seq#:28; N Pos. 12
Seq#:29; N Pos. 11
Seq#:30; N Pos. 11
Seq#:33; N Pos. 4,5,6,7,8,9,10,11,12,22,23,24,25,26,27
Seq#:92; N Pos. 7,8,10,11,12,14,15
Seq#:109; N Pos. 20,21,22,23,24
Seq#:110; N Pos. 25,26,27,28,29
Seq#:112; N Pos. 20,21,22,23,24
Seq#:113; N Pos. 25,26,27,28,29
Seq#:114; N Pos. 13,14
Seq#:115; N Pos. 13
Seq#:132; N Pos. 6950
Seq#:160; N Pos. 1326
Seq#:162; N Pos. 1102,3080
Seq#:171; N Pos. 1,2,3,4,5,6
Seq#:172; N Pos. 1,2,3,4,5,6,7,8
Seq#:173; N Pos. 1,2,3,4,5,6,7
Seq#:179; N Pos. 2263
Seq#:244; N Pos. 1
Seq#:274; N Pos. 1
Seq#:279; N Pos. 1
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